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PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Dahlquist, Anders
Stahl, Ulf
Lenman, Marit
Banas, Antoni
Ronne, Hans

<120> A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant DNA molecules encoding these enzymes

<130> BASFnae337799PCT1-15

<140> US 09/537,710

<141> 2000-03-30

<150> EP 99106656.4
<151> 1999-04-01

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Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
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Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65                  70                  75                  80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
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Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
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Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
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Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
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Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
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Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
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Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
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<212> PRT

<213> Arabidopsis thaliana

<400> 6

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Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
     50                  55                  60

Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
 65                  70                  75                  80

Gln Tyr Val Thr Glu Arg Ile Thr Gly Pro Leu Pro Asp Pro Pro Gly
                 85                  90                  95

Val Lys Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe
            100                 105                 110

Ile Pro Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln
        115                 120                 125

Cys Ala Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Gly
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Glu Val Tyr Lys Arg Pro Leu Cys Trp Val Glu His Met Ser Leu Asp
145                 150                 155                 160

Asn Glu Thr Gly Leu Asp Pro Ala Gly Ile Arg Val Arg Ala Val Ser
                165                 170                 175

Gly Leu Val Ala Ala Asp Tyr Phe Ala Pro Gly Tyr Phe Val Trp Ala
            180                 185                 190

Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
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Tyr Met Ala Ala Tyr Asp Trp Arg Leu Ser Phe Gln Asn Thr Glu Val
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Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val
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Ser Thr Asn Gly Gly Lys Lys Ala Val Ile Val Pro His Ser Met Gly
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Val Leu Tyr Phe Leu His Phe Met Lys Trp Val Glu Ala Pro Ala Pro
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Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala
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Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala
    290                 295                 300

Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile
305                 310                 315                 320

Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln
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His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
            340                 345                 350

Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
        355                 360                 365

Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
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Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
385                 390                 395                 400

Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
                405                 410                 415

Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
            420                 425                 430

Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
        435                 440                 445

Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
    450                 455                 460

Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
465                 470                 475                 480

Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
                485                 490                 495

Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
            500                 505                 510

Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
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Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
    530                 535                 540

Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
545                 550                 555                 560

Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
                565                 570                 575

Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
            580                 585                 590

Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
        595                 600                 605

His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
    610                 615                 620

Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
625                 630                 635                 640

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
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His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
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<213> Zea mays

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<223> n= a or g or c or t/u
<221> Unsure
<222> 1...643
<223> Xaa = unknown

<400> 7

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gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga   96
Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
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            20                  25                  30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg   144
Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
         35                  40                  45

aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc   192
Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
     50                  55                  60

acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att   240
Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65                  70                  75                  80

gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt   288
Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
                 85                  90                  95

ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa   336
Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
            100                 105                 110

ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att   384
Leu Lys Leu Xaa Pro Met Gly Ser Xaa Arg Ser Ala Asp Pro Phe Ile
        115                 120                 125

gcg ttc caa agt gtc ctg cctgagtgca actctggatt ttgcttaaat          432
Ala Phe Gln Ser Val Leu
    130

attgtaattt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgccaa 492

tgcgatacga tgttgtaccg ctattttcag cattgtatat taaactgtac aggtgtaagt 552

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gcagtgcccc aagcnaaaaa aaaaaaaaaa a                                 643


<210> 8
<211> 115
<212> PRT
<213> Zea mays

<400> 8

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Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
             20                  25                  30
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Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
         35                  40                  45

Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
     50                  55                  60

Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65                  70                  75                  80

Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
                 85                  90                  95

Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
            100                 105                 110

Leu Lys Leu
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<211> 616
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<400> 9

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<212> DNA
<213> Arabidopsis thaliana

<400> 10

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<212> DNA
<213> Arabidopsis thaliana

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<213> Lycopersicon esculentum

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<211> 623
<212> PRT
<213> Schizosaccharomyces pombe

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Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
50 55 60

Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala
65 70 75 80

Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
85 90 95

Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
100 105 110

Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
115 120 125

Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser

```
    130                 135                 140

Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
145                 150                 155                 160

Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
                165                 170                 175

Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
            180                 185                 190

Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
        195                 200                 205

Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
    210                 215                 220

Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala
225                 230                 235                 240

Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
                245                 250                 255

Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
            260                 265                 270

Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
        275                 280                 285

Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
    290                 295                 300

Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
305                 310                 315                 320

Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
                325                 330                 335

Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
            340                 345                 350

Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
        355                 360                 365

Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
    370                 375                 380

Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
385                 390                 395                 400

Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
```

405 410 415

Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
420 425 430

Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
435 440 445

Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
450 455 460

Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
465 470 475 480

Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
485 490 495

Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
500 505 510

Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
515 520 525

Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
530 535 540

Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
610 615 620

<210> 14
<211> 432
<212> PRT
<213> Arabidopsis thaliana

<400> 14
Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val
1 5 10 15

```
Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr
             20                  25                  30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg
         35                  40                  45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu
     50                  55                  60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp
 65                  70                  75                  80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met
                 85                  90                  95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly
            100                 105                 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr
        115                 120                 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val
    130                 135                 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu
145                 150                 155                 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro
                165                 170                 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu
            180                 185                 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His
        195                 200                 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro
    210                 215                 220

Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro
225                 230                 235                 240

Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr
                245                 250                 255

Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg
            260                 265                 270

Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His
        275                 280                 285
```

```
Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala
    290                 295                 300

Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
305                 310                 315                 320

Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
                325                 330                 335

Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
            340                 345                 350

Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
        355                 360                 365

Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
    370                 375                 380

Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
385                 390                 395                 400

Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
                405                 410                 415

Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
            420                 425                 430
```

<210> 15
<211> 552
<212> PRT
<213> Arabidopsis thaliana

<400> 15

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Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala
  1               5                  10                  15

Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr
             20                  25                  30

Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly
         35                  40                  45

Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr
     50                  55                  60

Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr
 65                  70                  75                  80
```

```
Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp
                 85                  90                  95

Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser
            100                 105                 110

Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro
        115                 120                 125

Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly
    130                 135                 140

Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser
145                 150                 155                 160

Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu
                165                 170                 175

Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe
            180                 185                 190

Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu
        195                 200                 205

Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His
    210                 215                 220

Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu
225                 230                 235                 240

Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser
                245                 250                 255

Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp
            260                 265                 270

Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr
        275                 280                 285

His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys
    290                 295                 300

Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile
305                 310                 315                 320

Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly
                325                 330                 335

Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met
            340                 345                 350
```

```
Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile
        355                 360                 365

Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro
    370                 375                 380

Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val
385                 390                 395                 400

Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe
                405                 410                 415

Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile
            420                 425                 430

Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val
        435                 440                 445

Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His
    450                 455                 460

Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr
465                 470                 475                 480

Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His
                485                 490                 495

Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly
            500                 505                 510

Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile
        515                 520                 525

Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val
    530                 535                 540

Trp Glu Leu Asp Lys Ser Gly Tyr
545                 550
```

<210> 16
<211> 387
<212> PRT
<213> Arabidopsis thaliana

<400> 16

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Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro Gly Asn Gly Gly
  1               5                  10                  15

Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val
             20                  25                  30
```

```
Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp
         35                  40                  45

Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg
     50                  55                  60

Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp
 65                  70                  75                  80

Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser
                 85                  90                  95

Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser
            100                 105                 110

Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val
        115                 120                 125

Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu
    130                 135                 140

Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp
145                 150                 155                 160

Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro
                165                 170                 175

Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe
            180                 185                 190

Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe
        195                 200                 205

Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr
    210                 215                 220

Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu
225                 230                 235                 240

Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
                245                 250                 255

Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
            260                 265                 270

Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile
        275                 280                 285

Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
    290                 295                 300
```

```
Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
305                 310                 315                 320

Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe
                325                 330                 335

Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
            340                 345                 350

Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
        355                 360                 365

Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
    370                 375                 380

Lys Glu Ile
385
```

<210> 17
<211> 389
<212> PRT
<213> Arabidopsis thaliana

<400> 17

```
Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
  1               5                  10                  15

Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
             20                  25                  30

Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
         35                  40                  45

Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
     50                  55                  60

Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
 65                  70                  75                  80

Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
                 85                  90                  95

Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
            100                 105                 110

Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
        115                 120                 125

Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
```

```
    130                 135                 140

Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
145                 150                 155                 160

Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys
                165                 170                 175

Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
            180                 185                 190

Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
        195                 200                 205

Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
    210                 215                 220

Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
225                 230                 235                 240

Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
                245                 250                 255

Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
            260                 265                 270

Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
        275                 280                 285

Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
    290                 295                 300

Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
305                 310                 315                 320

Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
                325                 330                 335

Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
            340                 345                 350

Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
        355                 360                 365

Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
    370                 375                 380

Gly Ile Phe Glu Trp
385

<210> 18
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<211> 402
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (120)..(401)

<221> Unsure
<222> 1..401
<223> n is c, g, a, t or u.

<221> Unsure
<222> 1..401
<223> Xaa = unknown

<400> 18

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ctggacgaga tttgacaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagat 119

atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167
Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
1 5 10 15

cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215
Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
20 25 30

gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg 263
Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp
35 40 45

tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311
Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
50 55 60

tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359
Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
65 70 75 80

cag tat gta acg gag ccg aat cac gng tcc ttt gcc tta ccc g 402
Gln Tyr Val Thr Glu Pro Asn His Xaa Ser Phe Ala Leu Pro
85 90

<210> 19
<211> 516
<212> DNA
<213> Neurospora crassa

<220>
<221> Unsure
<222> 1..516
<223> n is g, c, a, t, or u.

<400> 19

ggtggcgaag acganggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
accctctaga gacacgacta ccnttgcacc cagcctcaag gtntacngtt tntatgggta 120
ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcatc 180
tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggt gtgattttgg 240
gcgaaggcga tggcacagtg aaccttatga gtttggggta cctgtgcaat aaggggtgga 300
aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
cagaacggtt caatccgaga ggagggccga atacggcgga cttaaatatg tagaaaaggt 420
tgaaatttat gaagagtaat taaatacggc acataggtta ctcaatagta tgactaatta 480
aaaaaaaatt ttttttctaa aaaaaaaaaa aaaaaa 516

<210> 20
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of artificial sequence: PCR primer

<400> 20
tctccatctt ctgcaaaacc t 21

<210> 21
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Description of artificial sequence: PCR primer

<400> 21
cctgtcaaaa accttctcct c 21